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<110>  Eisai Co., Ltd.


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<151>  2003-01-24


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Leu Gln  Glu Gly Glu Val Arg  Ile Ile Pro Leu Glu  Gln Cys Gln

  1010    1015    1020

Ser Tyr  Phe Asp Met Lys Thr  Ile Thr Asn Arg Met  Ile Cys Ala

  1025    1030    1035

Gly Tyr  Glu Ser Gly Thr Val  Asp Ser Cys Met Gly  Asp Ser Gly

  1040    1045    1050

Gly Pro  Leu Val Cys Glu Arg  Pro Gly Gly Gln Trp  Thr Leu Phe

  1055    1060    1065

Gly Leu  Thr Ser Trp Gly Ser  Val Cys Phe Ser Lys  Val Leu Gly

  1070    1075    1080

Pro Gly  Val Tyr Ser Asn Val  Ser Tyr Phe Val Gly  Trp Ile Glu

  1085    1090    1095

Arg Gln  Ile Tyr Ile Gln Thr  Phe Leu Gln Lys Lys  Ser Gln Gly
    1100             1105             1110

<210> 4

<211> 1042

<212> PRT

<213> Homo sapiens

<400> 4

Met Lys Gln Ser Pro Ala Leu Ala Pro Glu Glu Arg Tyr Arg Arg Ala
1             5                 10                15

Gly Ser Pro Lys Pro Val Leu Arg Ala Asp Asp Asn Asn Met Gly Asn
            20                25                30

Gly Cys Ser Gln Lys Leu Ala Thr Ala Asn Leu Leu Arg Phe Leu Leu
        35                40                45

Leu Val Leu Ile Pro Cys Ile Cys Ala Leu Val Leu Leu Leu Val Ile
    50                55                60

Leu Leu Ser Tyr Val Gly Thr Leu Gln Lys Val Tyr Phe Lys Ser Asn
65                70                75                80

Gly Ser Glu Pro Leu Val Thr Asp Gly Glu Ile Gln Gly Ser Asp Val

        85                90                95

Ile Leu Thr Asn Thr Ile Tyr Asn Gln Ser Thr Val Val Ser Thr Ala
        100             105            110

His Pro Asp Gln His Val Pro Ala Trp Thr Thr Asp Ala Ser Leu Pro
        115             120            125

Gly Asp Gln Ser His Arg Asn Thr Ser Ala Cys Met Asn Ile Thr His
        130             135            140

Ser Gln Cys Gln Met Leu Pro Tyr His Ala Thr Leu Thr Pro Leu Leu
145             150            155           160

Ser Val Val Arg Asn Met Glu Met Glu Lys Phe Leu Lys Phe Phe Thr
          165            170           175

Tyr Leu His Arg Leu Ser Cys Tyr Gln His Ile Met Leu Phe Gly Cys
        180             185          190

Thr Leu Ala Phe Pro Glu Cys Ile Ile Asp Gly Asp Asp Ser His Gly
        195             200          205

Leu Leu Pro Cys Arg Ser Phe Cys Glu Ala Ala Lys Glu Gly Cys Glu
        210             215          220

Ser Val Leu Gly Met Val Asn Tyr Ser Trp Pro Asp Phe Leu Arg Cys

225 230 235 240

Ser Gln Phe Arg Asn Gln Thr Glu Ser Ser Asn Val Ser Arg Ile Cys

245 250 255

Phe Ser Pro Gln Gln Glu Asn Gly Lys Gln Leu Leu Cys Gly Arg Gly

260 265 270

Glu Asn Phe Leu Cys Ala Ser Gly Ile Cys Ile Pro Gly Lys Leu Gln

275 280 285

Cys Asn Gly Tyr Asn Asp Cys Asp Asp Trp Ser Asp Glu Ala His Cys

290 295 300

Asn Cys Ser Glu Asn Leu Phe His Cys His Thr Gly Lys Cys Leu Asn

305 310 315 320

Tyr Ser Leu Val Cys Asp Gly Tyr Asp Asp Cys Gly Asp Leu Ser Asp

325 330 335

Glu Gln Asn Cys Asp Cys Asn Pro Thr Thr Glu His Arg Cys Gly Asp

340 345 350

Gly Arg Cys Ile Ala Met Glu Trp Val Cys Asp Gly Asp His Asp Cys

355 360 365

Val Asp Lys Ser Asp Glu Val Asn Cys Ser Cys His Ser Gln Gly Leu
    370                375           380

Val Glu Cys Arg Asn Gly Gln Cys Ile Pro Ser Thr Phe Gln Cys Asp
385            390           395           400

Gly Asp Glu Asp Cys Lys Asp Gly Ser Asp Glu Glu Asn Cys Ser Val
        405           410           415

Ile Gln Thr Ser Cys Gln Glu Gly Asp Gln Arg Cys Leu Tyr Asn Pro
        420           425          430

Cys Leu Asp Ser Cys Gly Gly Ser Ser Leu Cys Asp Pro Asn Asn Ser
        435           440          445

Leu Asn Asn Cys Ser Gln Cys Glu Pro Ile Thr Leu Glu Leu Cys Met
        450           455          460

Asn Leu Pro Tyr Asn Ser Thr Ser Tyr Pro Asn Tyr Phe Gly His Arg
465            470           475          480

Thr Gln Lys Glu Ala Ser Ile Ser Trp Glu Ser Ser Leu Phe Pro Ala
        485           490          495

Leu Val Gln Thr Asn Cys Tyr Lys Tyr Leu Met Phe Phe Ser Cys Thr

                  500                    505                    510


Ile Leu Val Pro Lys Cys Asp Val Asn Thr Gly Glu Arg Ile Pro Pro
        515                    520                    525


Cys Arg Ala Leu Cys Glu His Ser Lys Glu Arg Cys Glu Ser Val Leu
        530                    535                    540


Gly Ile Val Gly Leu Gln Trp Pro Glu Asp Thr Asp Cys Ser Gln Phe
545                    550                    555                    560


Pro Glu Glu Asn Ser Asp Asn Gln Thr Cys Leu Met Pro Asp Glu Tyr
                  565                    570                    575


Val Glu Glu Cys Ser Pro Ser His Phe Lys Cys Arg Ser Gly Gln Cys
             580                    585                    590


Val Leu Ala Ser Arg Arg Cys Asp Gly Gln Ala Asp Cys Asp Asp Asp
        595                    600                    605


Ser Asp Glu Glu Asn Cys Gly Cys Lys Glu Arg Asp Leu Trp Glu Cys
        610                    615                    620


Pro Ser Asn Lys Gln Cys Leu Lys His Thr Val Ile Cys Asp Gly Phe
625                    630                    635                    640

Pro Asp Cys Pro Asp Tyr Met Asp Glu Lys Asn Cys Ser Phe Cys Gln
                645                        650              655

Asp Asp Glu Leu Glu Cys Ala Asn His Ala Cys Val Ser Arg Asp Leu
          660                  665              670

Trp Cys Asp Gly Glu Ala Asp Cys Ser Asp Ser Ser Asp Glu Trp Asp
          675                  680              685

Cys Val Thr Leu Ser Ile Asn Val Asn Ser Ser Ser Phe Leu Met Val
          690                  695              700

His Arg Ala Ala Thr Glu His His Val Cys Ala Asp Gly Trp Gln Glu
705              710              715              720

Ile Leu Ser Gln Leu Ala Cys Lys Gln Met Gly Leu Gly Glu Pro Ser
              725              730              735

Val Thr Lys Leu Ile Gln Glu Gln Glu Lys Glu Pro Arg Trp Leu Thr
              740              745              750

Leu His Ser Asn Trp Glu Ser Leu Asn Gly Thr Thr Leu His Glu Leu
          755                  760              765

Leu Val Asn Gly Gln Ser Cys Glu Ser Arg Ser Lys Ile Ser Leu Leu
          770                  775              780

Cys Thr Lys Gln Asp Cys Gly Arg Arg Pro Ala Ala Arg Met Asn Lys
785               790             795             800

Arg Ile Leu Gly Gly Arg Thr Ser Arg Pro Gly Arg Trp Pro Trp Gln
           805            810           815

Cys Ser Leu Gln Ser Glu Pro Ser Gly His Ile Cys Gly Cys Val Leu
         820           825           830

Ile Ala Lys Lys Trp Val Leu Thr Val Ala His Cys Phe Glu Gly Arg
     835           840          845

Glu Asn Ala Ala Val Trp Lys Val Val Leu Gly Ile Asn Asn Leu Asp
    850          855           860

His Pro Ser Val Phe Met Gln Thr Arg Phe Val Lys Thr Ile Ile Leu
865           870          875           880

His Pro Arg Tyr Ser Arg Ala Val Val Asp Tyr Asp Ile Ser Ile Val
         885          890          895

Glu Leu Ser Glu Asp Ile Ser Glu Thr Gly Tyr Val Arg Pro Val Cys
         900          905         910

Leu Pro Asn Pro Glu Gln Trp Leu Glu Pro Asp Thr Tyr Cys Tyr Ile

915     920     925

Thr Gly Trp Gly His Met Gly Asn Lys Met Pro Phe Lys Leu Gln Glu

930     935    940

Gly Glu Val Arg Ile Ile Ser Leu Glu His Cys Gln Ser Tyr Phe Asp

945    950    955    960

Met Lys Thr Ile Thr Thr Arg Met Ile Cys Ala Gly Tyr Glu Ser Gly

965    970    975

Thr Val Asp Ser Cys Met Gly Asp Ser Gly Gly Pro Leu Val Cys Glu

980    985    990

Lys Pro Gly Gly Arg Trp Thr Leu Phe Gly Leu Thr Ser Trp Gly Ser

995    1000    1005

Val Cys Phe Ser Lys Val Leu Gly Pro Gly Val Tyr Ser Asn Val Ser

1010    1015    1020

Tyr Phe Val Glu Trp Ile Lys Arg Gln Ile Tyr Ile Gln Thr Phe Leu

1025    1030    1035    1040

Leu Asn

<210> 5

<211> 26

<212> DNA

<213> Artificial Sequence


<220>

<223> Description of Artificial Sequence:adapter for

cDNA amplification


<400> 5

cagctccaca acctacatca ttccgt                                          26



<210> 6

<211> 12

<212> DNA

<213> Artificial Sequence


<220>

<223> Description of Artificial Sequence:adapter for

cDNA amplification


<400> 6

acggaatgat gt                                                        12

<210> 7

<211> 26

<212> DNA

<213> Artificial Sequence


<220>

<223> Description of Artificial Sequence:adapter for

cDNA amplification


<400> 7

gtccatcttc tctctgagac tctggt                                    26




<210> 8

<211> 12

<212> DNA

<213> Artificial Sequence


<220>

<223> Description of Artificial Sequence:adapter for

cDNA amplification


<400> 8

accagagtct ca                                                   12

<210> 9

<211> 26

<212> DNA

<213> Artificial Sequence


<220>

<223> Description of Artificial Sequence:adapter for
    cDNA amplification


<400> 9

ctgatgggtg tcttctgtga gtgtgt                                    26



<210> 10

<211> 12

<212> DNA

<213> Artificial Sequence


<220>

<223> Description of Artificial Sequence:adapter for
    cDNA amplification


<400> 10

acacactcac ag                                                    12

<210> 11

<211> 26

<212> DNA

<213> Artificial Sequence


<220>

<223> Description of Artificial Sequence:adapter for

cDNA amplification


<400> 11

ccagcatcga gaatcagtgt gacagt                                        26



<210> 12

<211> 12

<212> DNA

<213> Artificial Sequence


<220>

<223> Description of Artificial Sequence:adapter for

cDNA amplification


<400> 12

actgtcacac tg                                                      12

<210> 13

<211> 26

<212> DNA

<213> Artificial Sequence


<220>

<223> Description of Artificial Sequence:adapter for

cDNA amplification


<400> 13

gtcgatgaac ttcgactgtc gatcgt                                26



<210> 14

<211> 12

<212> DNA

<213> Artificial Sequence


<220>

<223> Description of Artificial Sequence:adapter for

cDNA amplification


<400> 14

acgatcgaca gt                                               12